

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/551,300A  
Source: 1FWP  
Date Processed by STIC: 2/10/07

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 02/10/2007

PATENT APPLICATION: US/10/551,300A

TIME: 09:28:04

Input Set : E:\substitute seqlisting 10589-034.TXT

Output Set: N:\CRF4\02102007\J551300A.raw

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4 <110> APPLICANT: Trotta, Christopher R.
6 <120> TITLE OF INVENTION: TARGETING ENZYMES OF THE tRNA SPLICING
7   PATHWAY FOR IDENTIFICATION OF ANTI-FUNGAL AND/OR
8   ANTI-PROLIFERATIVE MOLECULES
10 <130> FILE REFERENCE: 10589-034-999
12 <140> CURRENT APPLICATION NUMBER: US/10/551,300A
13 <141> CURRENT FILING DATE: 2005-09-27
15 <150> PRIOR APPLICATION NUMBER: PCT/US2004/009590
16 <151> PRIOR FILING DATE: 2004-03-26
18 <150> PRIOR APPLICATION NUMBER: 60/458,067
19 <151> PRIOR FILING DATE: 2003-03-27
21 <160> NUMBER OF SEQ ID NOS: 4
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 465
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <223> OTHER INFORMATION: HsSen2p
33 <400> SEQUENCE: 1
34 Met Ala Glu Ala Val Phe His Ala Pro Lys Arg Lys Arg Arg Val Tyr
35 1 5 10 15
36 Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly
37 20 25 30
38 Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn
39 35 40 45
40 Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly
41 50 55 60
42 Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile
43 65 70 75 80
44 Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met
45 85 90 95
46 Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala
47 100 105 110
48 Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile
49 115 120 125
50 Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn
51 130 135 140
52 Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn
53 145 150 155 160
54 Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly Asp
55 165 170 175
56 Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys

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57          180          185          190
58 Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys
59          195          200          205
60 Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Cys Lys
61          210          215          220
62 Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser
63 225          230          235          240
64 Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu
65          245          250          255
66 Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala
67          260          265          270
68 Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg
69          275          280          285
70 Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Ala
71          290          295          300
72 Phe Phe Leu Val Tyr Ala Leu Gly Cys Leu Ser Ile Tyr Tyr Glu Lys
73 305          310          315          320
74 Glu Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln
75          325          330          335
76 Pro Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys
77          340          345          350
78 Gly Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Leu
79          355          360          365
80 Tyr Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile
81          370          375          380
82 Glu Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser
83 385          390          395          400
84 Trp Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys
85          405          410          415
86 Glu Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys
87          420          425          430
88 Glu Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val
89          435          440          445
90 Ile Leu Ser Arg Trp Val Ser Ser Arg Glu Arg Ser Asp Gln Asp Asp
91          450          455          460
92 Leu
93 465
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 448
98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
101 <220> FEATURE:
102 <223> OTHER INFORMATION: HsSen2 variant
104 <400> SEQUENCE: 2
105 Met Ala Glu Ala Val Phe His Ala Pro Lys Arg Lys Arg Arg Val Tyr
106 1          5          10          15
107 Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly
108          20          25          30
109 Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn

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```

110          35          40          45
111 Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly
112          50          55          60
113 Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile
114 65          70          75          80
115 Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met
116          85          90          95
117 Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala
118          100          105          110
119 Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile
120          115          120          125
121 Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn
122          130          135          140
123 Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn
124 145          150          155          160
125 Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly Asp
126          165          170          175
127 Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys
128          180          185          190
129 Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys
130          195          200          205
131 Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Cys Lys
132          210          215          220
133 Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser
134 225          230          235          240
135 Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu
136          245          250          255
137 Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala
138          260          265          270
139 Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg
140          275          280          285
141 Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Glu
142          290          295          300
143 Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln Pro
144 305          310          315          320
145 Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys Gly
146          325          330          335
147 Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Leu Tyr
148          340          345          350
149 Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile Glu
150          355          360          365
151 Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser Trp
152          370          375          380
153 Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys Glu
154 385          390          395          400
155 Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys Glu
156          405          410          415
157 Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val Ile
158          420          425          430

```

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159 Leu Ser Arg Trp Val Ser Ser Arg Glu Arg Ser Asp Gln Asp Asp Leu
160      435                      440                      445
163 <210> SEQ ID NO: 3
164 <211> LENGTH: 377
165 <212> TYPE: PRT
166 <213> ORGANISM: Saccharomyces cerevisiae
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Sc Sen2p
171 <400> SEQUENCE: 3
172 Met Ser Lys Gly Arg Val Asn Gln Lys Arg Tyr Lys Tyr Pro Leu Pro
173 1      5                      10                      15
174 Ile His Pro Val Asp Asp Leu Pro Glu Leu Ile Leu His Asn Pro Leu
175      20                      25                      30
176 Ser Trp Leu Tyr Trp Ala Tyr Arg Tyr Tyr Lys Ser Thr Asn Ala Leu
177      35                      40                      45
178 Asn Asp Lys Val His Val Asp Phe Ile Gly Asp Thr Thr Leu His Ile
179      50                      55                      60
180 Thr Val Gln Asp Asp Lys Gln Met Leu Tyr Leu Trp Asn Asn Gly Phe
181 65      70                      75                      80
182 Phe Gly Thr Gly Gln Phe Ser Arg Ser Glu Pro Thr Trp Lys Ala Arg
183      85                      90                      95
184 Thr Glu Ala Arg Leu Gly Leu Asn Asp Thr Pro Leu His Asn Arg Gly
185      100                     105                     110
186 Gly Thr Lys Ser Asn Thr Glu Thr Glu Met Thr Leu Glu Lys Val Thr
187      115                     120                     125
188 Gln Gln Arg Arg Leu Gln Arg Leu Glu Phe Lys Lys Glu Arg Ala Lys
189      130                     135                     140
190 Leu Glu Arg Glu Leu Leu Glu Leu Arg Lys Lys Gly Gly His Ile Asp
191 145      150                     155                     160
192 Glu Glu Asn Ile Leu Leu Glu Lys Gln Arg Glu Ser Leu Arg Lys Phe
193      165                     170                     175
194 Lys Leu Lys Gln Thr Glu Asp Val Gly Ile Val Ala Gln Gln Gln Asp
195      180                     185                     190
196 Ile Ser Glu Ser Asn Leu Arg Asp Glu Asp Asn Asn Leu Leu Asp Glu
197      195                     200                     205
198 Asn Gly Asp Leu Leu Pro Leu Glu Ser Leu Glu Leu Met Pro Val Glu
199      210                     215                     220
200 Ala Met Phe Leu Thr Phe Ala Leu Pro Val Leu Asp Ile Ser Pro Ala
201 225      230                     235                     240
202 Cys Leu Ala Gly Lys Leu Phe Gln Phe Asp Ala Lys Tyr Lys Asp Ile
203      245                     250                     255
204 His Ser Phe Val Arg Ser Tyr Val Ile Tyr His His Tyr Arg Ser His
205      260                     265                     270
206 Gly Trp Cys Val Arg Ser Gly Ile Lys Phe Gly Cys Asp Tyr Leu Leu
207      275                     280                     285
208 Tyr Lys Arg Gly Pro Pro Phe Gln His Ala Glu Phe Cys Val Met Gly
209      290                     295                     300
210 Leu Asp His Asp Val Ser Lys Asp Tyr Thr Trp Tyr Ser Ser Ile Ala
211 305      310                     315                     320

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Input Set : E:\substitute seqlisting 10589-034.TXT

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212 Arg Val Val Gly Gly Ala Lys Lys Thr Phe Val Leu Cys Tyr Val Glu  
213                   325                   330                   335  
214 Arg Leu Ile Ser Glu Gln Glu Ala Ile Ala Leu Trp Lys Ser Asn Asn  
215                   340                   345                   350  
216 Phe Thr Lys Leu Phe Asn Ser Phe Gln Val Gly Glu Val Leu Tyr Lys  
217                   355                   360                   365  
218 Arg Trp Val Pro Gly Arg Asn Arg Asp  
219                   370                   375  
222 <210> SEQ ID NO: 4  
223 <211> LENGTH: 5  
224 <212> TYPE: PRT  
225 <213> ORGANISM: Artificial Sequence  
227 <220> FEATURE:  
228 <223> OTHER INFORMATION: Motif of the active site for the 5' splice site of yeast  
229       and archael tRNA splicing endonuclease  
231 <400> SEQUENCE: 4  
232 Tyr Arg Gly Gly Tyr  
233   1                   5

VERIFICATION SUMMARY

DATE: 02/10/2007

PATENT APPLICATION: US/10/551,300A

TIME: 09:28:05

Input Set : E:\substitute seqlisting 10589-034.TXT

Output Set: N:\CRF4\02102007\J551300A.raw